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Generated version 4.5

Run on: April 24 2002 at 14:53

Sequence: PIR:68:\*

Scoring table: BL250M2

Gap: 10.0 , Salign: 9.5

Searched: 21941 seqs, 76174532 residues

total number of hits satisfying chosen parameters: 21941

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.08

Maximum Match 10.0

Listing first 45 summaries

Database : PIR:68:\*

1: pirl1:\*

2: pirl2:\*

3: pirl3:\*

4: pirl4:\*

5: pirl5:\*

6: pirl6:\*

7: pirl7:\*

8: pirl8:\*

9: pirl9:\*

10: pirl10:\*

11: pirl11:\*

12: pirl12:\*

13: pirl13:\*

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15: pirl15:\*

16: pirl16:\*

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242: pirl242:\*

243: pirl243:\*

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245: pirl245:\*

246: pirl246:\*

247: pirl









Query Match 18 88%; Score 176.5; DR 1; length 425; Best Local Similarity 30.9%; Pred. No. 3.6e-06; Matches 50; Conservative 25; Mismatches 68; Indexes 19; Gaps 10.

QY 4 CPGGKTHQNNNSGCKKKGTYVYNNPQGQGQKKGKESGCSFVASHENRHCISG 62

DB 33 GSTGLYH--SGECKAKNLGEWQEP-GANG-TVEPCLNVTEDVSVATEPKC 87

QY 63 SKKREMGWWEISSCIVETKETWACKKNNQFHYWSELPWENQSLQNLQVNLQV 126

DB 88 TPG---IGQSMASQCFVAVWVH---AVGQYQVQVPGHCPACSVCEVSGVWFGQ 141

QY 121 KPNWV TPHCTTIE HEVVSNSHPEFLE; PFLVLE 157

DB 142 KUNTWQFPEKPGTYSDFANVNDPQIPCPVCFDPERQJRECTP 183

RESULT 11

148854

Query Match 18 79%; Score 176.5; DR 2; length 459; Best Local Similarity 31.1%; Pred. No. 4.1e-06; Matches 50; Conservative 20; Mismatches 77; Indexes 14; Gaps 8;

DB 25 QTSQFYYDVRKAMQCKPFGVVKH-NKTSDTWVNECEASMYTUVWQHICLTS 83

QY 64 KCKREMGWWEISSCIVETKETWACKKNNQFHYWSELPWENQSLQNLQVNLQV 122

DB 82 HCEPNQGLRKKEGTAESDTVTCKEGK---HCTSKDENCAGCQTCIPGCMEMATT 139

QY 123 NIVC-TCHAOFFIREN---ECVSCSNK--KSLE 150

DB 140 DVVCHQIPWGGFESSNQSLFCKVWTSCKKNE 173

RESULT 13

1521 75

Query Match 17.8%; Score 167.5; DR 2; length 405; Best Local Similarity 29.9%; Pred. No. 1.3e-05; Matches 46; Conservative 23; Mismatches 72; Indexes 13; Gaps 7;

DB 26 CSDKQYHL--DGQCGCQGKPSRSHCIAL-EKTOUCHPDSGERSAUNNREKHOHR 81

QY 64 KCKREMGWWEISSCIVETKETWACKKNNQFHYWSELPWENQSLQNLQVNLQV 122

DB 82 HCEPNQGLRKKEGTAESDTVTCKEGK---HCTSKDENCAGCQTCIPGCMEMATT 139

QY 123 NIVC-TCHAOFFIREN---ECVSCSNK--KSLE 150

DB 140 DVVCHQIPWGGFESSNQSLFCKVWTSCKKNE 173

RESULT 14

1521 75

Query Match 17.8%; Score 167.5; DR 2; length 405; Best Local Similarity 29.9%; Pred. No. 1.3e-05; Matches 46; Conservative 23; Mismatches 72; Indexes 13; Gaps 7;

DB 26 CSDKQYHL--DGQCGCQGKPSRSHCIAL-EKTOUCHPDSGERSAUNNREKHOHR 81

QY 64 KCKREMGWWEISSCIVETKETWACKKNNQFHYWSELPWENQSLQNLQVNLQV 122

DB 82 HCEPNQGLRKKEGTAESDTVTCKEGK---HCTSKDENCAGCQTCIPGCMEMATT 139

QY 123 NIVC-TCHAOFFIREN---ECVSCSNK--KSLE 150

DB 140 DVVCHQIPWGGFESSNQSLFCKVWTSCKKNE 173

Query Match 17.7%; Score 166.5; DR 2; length 349; Best Local Similarity 26.7%; Pred. No. 1.7e-05; Matches 46; Conservative 19; Mismatches 64; Indexes 43; Gaps 9;

DB 32 CKYTY--KRNHKGCGSFGVYASKRKGK--TNOQIVQGSGFTSRNNHHLACISN 87

QY 64 -KCKREMGWWEISSCIVETKETWACKKNNQFHYWSELPWENQSLQNLQVNLQV 127

DB 88 GRGNS--NOVFRSNTWTHNRCFCSPYY-----CILKGSGGKACVSN----- 131

QY 118 QPKKNTVCTCHAEFFRHEEVV---CSNQ-----KKSILKTKLQVQH 161

DB 132 -----KPKLQYVWSSHISLWV-----FIVYVIVSLLK-EFVNN 174

A; Cross-references: GB:MR3312, NIB:3153038

A; Note: sequence extracted from NIBI backbone (NCBIN:75206, NCBI:75207)

A; Note: this translation is not annotated in GenBank entry MUSM16A, release 113.0

R; Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chand, R.; Clark, R.A.; Howard, M.; Cockayne,

J. Immunol. 149, 3923-3926, 1992

A; Title: Economic structure and chromosomal mapping of the murine CD40 gene.

A; Reference number: A46515; MIPD:93094586

A; Accession: A46515

A; Status: preliminary, not compared with conceptual translation

A; Residues: 1-287, 'IV' <GRL>

A; Cross-references: G4: MR312, NIB:3153038; MIPD:93094586; 39: M94126

A; Experimental source: BALB/c, Liver

A; Note: sequence extracted from NIBI backbone (NCBI:120357)

C; Comment: For an alternative splice form, see PIR:RA46515.

C; Superfamily: C027 antigen, NGF receptor repeat, transmembrane protein

C; Keywords: alternative splicing; transmembrane protein

F; Int: 14455; MSA: B7T repeat; 1-repeat; homolog



